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<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

<400> SEQUENCE: 92

His Glu Gly Gly Phe Pro Pro Leu Leu Arg Arg Ala Ala Glu Asp
1 5 10 15

<210> SEQ ID NO 93
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<400> SEQUENCE: 93

Leu Ser Pro Val Trp Cys Leu Gln Trp Lys Leu Ser Gly Thr Asp
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<210> SEQ ID NO 94
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<400> SEQUENCE: 94

Lys Asn Thr Ile Val Tyr Thr Thr Lys Gln Val Gln Ser Cys Gln
1 5 10 15

<210> SEQ ID NO 95
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<212> TYPE: PRT
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

<400> SEQUENCE: 95

Asn Asn Glu Gln Phe Gln Trp Lys Ile Arg His Val Gly Pro Glu
1 5 10 15

<210> SEQ ID NO 96
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

<400> SEQUENCE: 96

Tyr Lys Gly Gly Tyr Glu Leu Val Lys Lys Ser Gln Thr Glu Leu
1 5 10 15

1. A method comprising:

processing amino acid information of a plurality of candidate peptide sequences using a machine learning HLA-peptide presentation prediction model to generate a plurality of presentation predictions, wherein each candidate peptide sequence of the plurality of candidate peptide sequences is encoded by a genome, transcriptome, or exome of a subject, or a pathogen or a virus in the subject;

wherein the plurality of presentation predictions comprises an HLA presentation prediction for each of the plurality of candidate peptide sequences, wherein